

Figure 1. Amplification of the PCR Positive $\alpha 10$ cDNA Insert

(drawing not to scale)

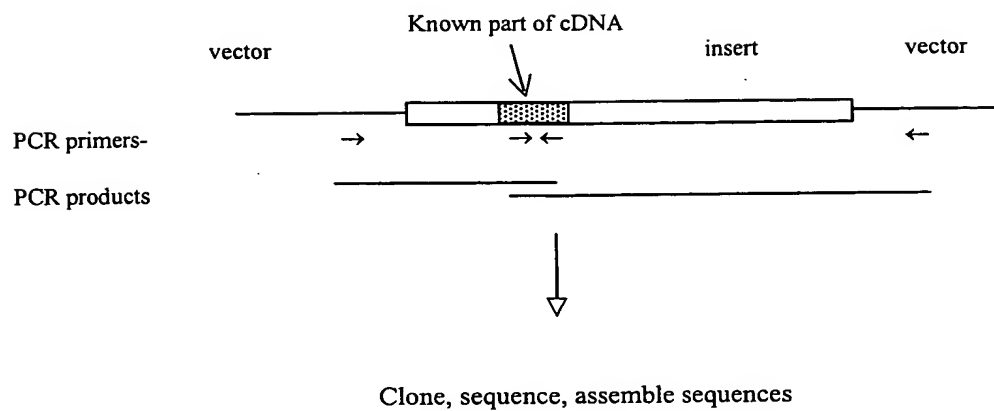


Figure 2. Assembled sequence of the $\alpha 10$ clone

```

1  taatacgact cactataggg cggccgcgga ggaaaatgtg tgtcagtaaa qcctggggaa
                                alpha10-1

61  gtgtgttttc aagtgaggg agtgttccat cgcacagaa gttttgaaga aaccagctcg
    alpha10-2

121 agatggagaa gtggaacag gtttgagaga tactggaggg ggcagagcag tgggatttag

181 aatccctggg tgaaagtctg gactctcgtg gcttatttgg gcccctctag catttggtga

241 gaggcaggca gactccaggt ccttgaaaag gggaggggtg aggagaaatt tgtcagcctg

301 gcgccagaag atagtaccg ttcactccat gccccttacc tcatgtgtcc ctgcaggcag
    alpha10-9                                alpha10-10

361 gccagggagg aactagagcc acagctagag caagagaagg cagacaccag gaggacactc

+2                                     * g
421 ataaggacag ggccccagcc ctgggagtgg aggggtgtgag cagaggccct gggactaggg

+2  l g w t t l l t d p p E C L G A E G R L
481 cctgggatgg acaaccctcc ttactgaccc tccagAGTGC CTGGGAGCTG AGGGCCGCT

+2  A L K L F R D L F A N Y T S A L R P V A
541 GGCTCTCAAG CTGTTCCGTG ACCTCTTTGC CAACTACACA AGTGCCCTGA GACCTGTGGC

+2  D T D Q T L N V T L E V T L S Q I I D M
601 AGACACAGAC CAGACTCTGA ATGTGACCCT GGAGGTGACA CTGTCCCAGA TCATCGACAT

+2  D E R D Q V L T L Y L W I R Q E W T D A
661 GGATGAACGG GACCAGGTGC TGACCCTGTA TCTGTGGATA CGGCAGGAGT GGACAGATGC

+2  Y L R W X P N A Y G G L D A I R I P S S
721 CTACCTACGA TGGGRCCCA ATGCCTATGG TGGCCTGGAT GCCATCCGA TCCCCAGCAG

+2  L V W R P D I V L Y N K
781 TCTTGTGTGG CGGCCAGACA TCGTACTCTA TAACAAGtac tgcctatctg ggcccctcct

841 ctctcttacc cctctctaga cttgccctta gctgtggggg tgtagtgatc ccctctccct

901 accacataac ctggttgcca cgctgccctg gaagcttttc cccaggaccc ttctaagctg

961 ccaagcactc agcccctcca tggcaccccc acttttaggt atcccaggcc agcccaggct

1021 gaacgtctcc tcggaaccta ctgtgtggtc cagggcagat gtctgaatca caagggcctc

1081 tctagggcac acttttagct ctaagtctct cagggctccc ccaagagcct gtctaaggg

1141 ctctttcctc caggacatag cctctggaa cactgcttta tgtctccttg accagttccg

1201 tgtctccag ccagcacata gctctgcata tttctctgg ggccttcta caagttttgc

1261 agatgtcccc caaggaagt cactgtgtgt cccggagcta cctctgggtt ctgcagaggg

```

1321 ctttttatac atcctctggc tacgtctgtg tcccttctgg gcccttcagg caccacccct
 1381 tccaggcctc gaaaggcagc ggggtctctct aggtgcactc caccctctgt gttgctttgt
 1441 tctgaaaaca agaatcaa ataacgaaaa aaaacaagca caagtttatt tatttatttg
 1501 agacacagtc tcgctctgtc gccaggtgtg gagtgcagtg gcgctatctc ggctcactgc
 1561 aagctccgcc tcccgggttc acgcaattct cctgcctcaa cctcccaa atactgggact
 1621 gcaggcaccc gccaccacgc ccagctagtt ttttgatttt ttagtagaga cgaggtttca
 1681 ccgtgttagc cagggtggtc tcgatctcct gacctcgtga tccgcccacc tcggcctccc
 1741 aaagtgtggt gattacaggc gtgagccacc gcaccagcc acaagcagaa gtttattaat
 1801 ctgctgtacc catcatggga gaggccttag ttcaaaagta tttctctctg aaggcagtga
 1861 cttaggggcc ttgcttaa atagaaattcaa gaaagagcca gtaagttata aatagtggca
 1921 agacaaaagga cagccacctt taaaaggcgg gaaaacgtgg aaagagggtg aaatctgttt
 1981 ccagattcct ctggcaccta ctggtgcctt ttggataagc aagtgtgtac tccagcaagg
 2041 aagggtgtgt gtcttgccat caggccagca gacgtgtggg ccaggtgtct ccctgcgtcg
 2101 tgagtgtctc gaacttaacg agcctcaata ttctggggag aagttttggt ttctttcagc
 2161 ccctgggggt ctgcctggg ctcccgccct ccgggggtgc tctcagggt ggacagccta

+2 A D A Q P P G S A S T
 2221 ggtgagccct gcccgcctg ccccagAGC CGACGCGCAG CCTCCAGGTT CCGCCAGCAC

+2 N V V L R H D G A V R W D A P A I T R S
 2281 CAACGTGGTC CTGCGCCACG ATGGCGCCGT GCGCTGGGAC GCGCCGGCCA TCACGCGCAG
 alpha10-3

+2 S C R V D V A A F P F D A Q H C G L T F
 2341 CTCGTGCCGC GTGGATGTAG CAGCCTTCCC GTTCGACGCC CAGCACTGCG GCCTGACGTT

+2 G S W T H G G H Q L D V R P R G A A A S
 2401 CGGCTCCTGG ACTCACGGCG GGCACCAACT GGATGTGCGG CCGCGGGCG CTGCAGCCAG
 alpha10-4

+2 L A D F V E N V E W R V L G M P A R R R
 2461 CCTGGCGGAC TTCGTGGAGA ACGTGGAGTG GCGCGTGCTG GGCATGCCGG CGCGGCGGCG
 alpha10-5*

+2 V L T Y G C C S E P Y P D V T F T L L L
 2521 CGTGCTCACC TACGGCTGCT GCTCCGAGCC CTACCCCGAC GTCACCTTCA CGCTGCTGCT
 alpha10-6*

+2 R R R A A A Y V C N L L L P C V L I S L
 2581 GCGCGCGCGC GCGCGGCCT ACGTGTGCAA CCTGCTGCTG CCCTGCGTGC TCATCTCGCT

+2 L A P L A F H L P A D S G E K V S L G V
 2641 GCTTGCGCCG CTCGCCTTCC ACCTACCTGC CGACTCAGGC GAGAAGGTGT CGCTGGGCGT

+2 T V L L A L T V F Q L L L A E S M P P A
 2701 CACCGTGCTG CTGGCGCTCA CCGTCTTCCA GTTGCTGCTG GCCGAGAGCA TGCCACCGGC

+2 E S V P L I G K Y Y M A T M T M V T F S
 2761 CGAGAGCGTG CCGCTCATCG GGAAGTACTA CATGGCCACT ATGACCATGG TCACATTCTC

+2 T A L T I L I T N L H Y C G P S V R P V
 2821 AACAGCACTC ACCATCCTTA TCACGAACCT GCATTACTGT GGTCCCAGTG TCCGCCCAGT

+2 P A W A R A L L L G H L A R G L C V R E
 2881 GCCAGCCTGG GCTAGGGCCC TCCTGCTGGG ACACCTGGCA CGGGGCCTGT GCGTGC GGGA

+2 R G E P C G Q S R P P E L S P S P Q S P
 2941 AAGAGGGGAG CCCTGTGGGC AGTCCAGGCC ACCTGAGTTA TCTCCTAGCC CCCAGTCGCC

+2 E G G A G P P A G P C H E P R C L C R Q
 3001 TGAAGGAGGG GCTGGCCCCC CAGCGGGCCC TTGCCACGAG CCACGATGTC TGTGCCGCCA

+2 E A L L H H V A T I A N T F R S H R A A
 3061 GGAAGCCCTA CTGCACCACG TAGCCACCAT TGCCAATACC TTCCGAGCC ACCGAGCTGC

+2 Q R C H E D W K R L A R V M D R F F L A
 3121 CCAGCGCTGC CATGAGGACT GGAAGCGCCT GGCCCGTGTG ATGGACCGCT TCTTCCTGGC

+2 I F F S M A L V M S L L V L V Q A L *
 3181 CATCTTCTTC TCCATGGCCC TGGTCATGAG CCTCCTGGTG CTGGTGCAGG ccctgtgagg

3241 gctgggacta agtcacaggg atctgctgca gccacagctc ctccagaaag ggacagccac

3301 ggccaagtgg ttgctggtct ttgggccagc cagtctctcc ccaactgctcc taagatcctg

3361 agacacttga cttcacaatc cacaagggag cactcattgt ctacacaccc taactaaagg

3421 aaqtccagaq cctgcccactc ccctaattcc aaaaaaaga ggaactctac aaaggccaag
 alpha10-7* alpha10-8*

3481 atcacagagt acagtcttgg agggacagaa ttgtttgtgc tgggtattgg agctctcagt

3541 ggggagcaca tgggttataa tgagaaactg aactgtactg ctgcatttcc tgtcttcctt

3601 cctaggtggc tgctttgcag ggctttggct gttaccttcc cctgctgagg ggctcagggg

3661 aaagggtcgg ggattctcag tcgagtttcc agagcaggag gccctacaga catttgcccc

3721 caaatccctg actcaataaa gtaagcgtgt acctaataaa aaaaaaaaaa aactcgactc

3781 tagattgcgg ccgcggtcat agctgtttcc tgatctgaat tcgtcgacaa gctt

Figure 3. Primers used to amplify unspliced cDNAs

Alpha10-1	GGAAAATGTGTGTGTCAGTAAAGC
Alpha10-2	GAAGTGTTTTTCAGAGTGAGG
Alpha10-3	CAGCACCAACGTGGTCC
Alpha10-4	GGCACCAACTGGATGTGC
Alpha10-5	CACGTTCTCCACGAAGTCC
Alpha10-6	CAGCCGTAGGTGAGCACG
Alpha10-7	TGGCAGGCTTTTGGACTTCC
Alpha10-8	TCTTGGCCTTTGTAGAGTTCC
Alpha10-9	TGGCGCCAGAAGATAGTACC
Alpha10-10	TCACTCCATGGCCCTTACC

Figure 4

```

      *           20           *           40           *           60
a10_human : MGLRSHHLSGLLLF--LLPAEGLCAEGRLALKLERDLFANYTSALRPVADTDQTLNVT : 58
a10_rat   : MGTRSHYLDLGLLL--FLPAEGLCAEGRLAHKLERDLFANYTSALRPVADTDQTLNVT : 58
a10_chicke : MGSAPLPACELALSLAGTVLAPGGAAQGRLAHKLHDLFANYSSALRPAEDTERALNVT : 60
a9_human  : MNWSHSCISFCWYFA-ASRLAAETADGKYAOKLENDLFEDYSNALRPVEDTDKVLNVT : 59
a9_rat    : MNRPHSCLSFCHWYFA-ASGIRAVETANGKYAOKLESDFEDYSSALRPVEDTDAVLNVT : 59

      *           80           *           100          *           120
a10_human : LEVTLSQLIDMDERNQVLTLYLWIRQEWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVL : 118
a10_rat   : LEVTLSQLIDMDERNQVLTLYLWIRQEWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVL : 118
a10_chicke : LQVTLSQLIDMDERNQVLTLYLWIRQEWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVL : 120
a9_human  : LQITLSQLIDMDERNQVLTLYLWIRQEWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVL : 119
a9_rat    : LQVTLSQLIDMDERNQVLTLYLWIRQEWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVL : 119

      *           140          *           160          *           180
a10_human : YNKADACPPGSASTNVVLRHGDGAVRWDAIPATRSSCRVDVAAPFDDAQCGLTFGSGWTHG : 178
a10_rat   : YNKADACPPGSASTNVVLRHGDGAVRWDAIPATRSSCRVDVAAPFDDAQCGLTFGSGWTHG : 178
a10_chicke : YNNADERFGGSMETNVVLRSDGHIMWDSPAITKSSCVVDVTFPFDDCCRLTFGSGWTYN : 180
a9_human  : YNKADDESSEPVTNVVLRDGLITWDAIPAITKSSCVVDVTFPFDDCCRLTFGSGWTYN : 179
a9_rat    : YNKADDESSEPVTNVVLRDGLITWDSPAITKSSCVVDVTFPFDDCCRLTFGSGWTYN : 179

      *           200          *           220          *           240
a10_human : GHOLDVPRGAAASLADFVENVEWRVLGMPARRRVLTYGCCSEPYPDVTFLLLRRAAAA : 238
a10_rat   : GHOLDVPRGTSASLADFVENVEWRVLGMPARRRVLTYGCCSEPYPDVTFLLLRRAAAA : 238
a10_chicke : GNOIDLNNLLDGLTDFVENVEWRVLGMPATRNVVLTYGCCSEPYPDVTFLLLRRAAA : 240
a9_human  : GNOVDIFNALDSGLSDFIEDVEVHGMPAVKKNVISYGCCSEPYPDVTFLLLRKRSSE : 239
a9_rat    : GNOVDIFNALDSGLSDFIEDVEVHGMPAVKKNVISYGCCSEPYPDVTFLLLRKRSSE : 239

      *           260          *           280          *           300
a10_human : YVCNLLPCVFIISLAPLAFHLPADSGEKVSLGVTVLLALTVFQLLLAESMPPAESVPLI : 298
a10_rat   : YVCNLLPCVFIISLAPLAFHLPADSGEKVSLGVTVLLALTVFQLLLAESMPPAESVPLI : 298
a10_chicke : YIFNLLPCVMISLAPLAFHLPADSGEKVSLGVTVLLALTVFQLLVAESMPPPSESVPLI : 300
a9_human  : YIVNLLPCVFIISLAPLAFHLPADSGEKVSLGVTILLAMTVFQLMVAETMPASENVPLI : 299
a9_rat    : YIVNLLPCVFIISLAPLAFHLPADSGEKVSLGVTILLAMTVFQLMVAETMPASENVPLI : 299

      *           320          *           340          *           360
a10_human : GKYYMATMIMVTFSTALTIIMNLIHYCGPSVRPVPANARALLGHLARGLGVRERGEPCG : 358
a10_rat   : GKYYMATMIMVTFSTALTIIMNLIHYCGPSVRPVPANARALLGHLARGLGVRERGEPCG : 358
a10_chicke : GKYYIATMIMITASTALTIIMNIHCCGPGARPVPWPARRLIHHLARALGVCEVGESCG : 360
a9_human  : GKYYIATMALITASTALTIIMNIHCCGAEARPVPHPWARRVILKYSRVLEFVYDVGESCL : 359
a9_rat    : GKYYIATMALITASTALTIIMNIHCCGAEARPVPHPWARRVILKYSRIIFVYDVGESCL : 359

      *           380          *           400          *           420
a10_human : QSRPPELSPSPQSPGEGAGPPAGPCHEPGLCHQ----- : 392
a10_rat   : QSKPLESAPSLQPP---PASAPGPCHEPGLCHQ----- : 389
a10_chicke : RFOREGTGGMGPRDPPGEGVEPGLGPRSRCLCHH----- : 394
a9_human  : SPHHSRERDHLTKVYSKLPESNLKAARNKDLSRKKDMNKRLKNDLGCGKNPQEAESYCA : 419
a9_rat    : SPRHSQEPQVTKVYSKLPESNLKTSRNKDLSRKKEVRKLLKNDLGYYGGIPQNTDSYCA : 419

      *           440          *           460          *           480
a10_human : --EALLHHVATIANFERSHRAAQRCHEDWKRLARVMDRFFLAIFESMALVMSLLVLVQAL : 450
a10_rat   : --EALLHHIASIAFERSHRAAQRCHEDWKRLARVMDRFFLGIFFCMALVMSLIVLQAL : 447
a10_chicke : --HAYLSSVGYIAGVRRRHRTAORRAAEWKKVAKVMDRFFMWVFFLMVFLMSVLVIGKAA : 452
a9_human  : QYKVLTRNIEYIAKCLKDKHKTSSKGSEWKKVAKVIDRFFMWIFFMVFVMTILITARAD : 479
a9_rat    : RYEFALAKNIEYIAKCLKDKHKTNSKGSEWKKVAKVIDRFFMWIFFMVFVMTVLIIARAD : 479

```

Figure 5. Pictorial representation of location of ESTs

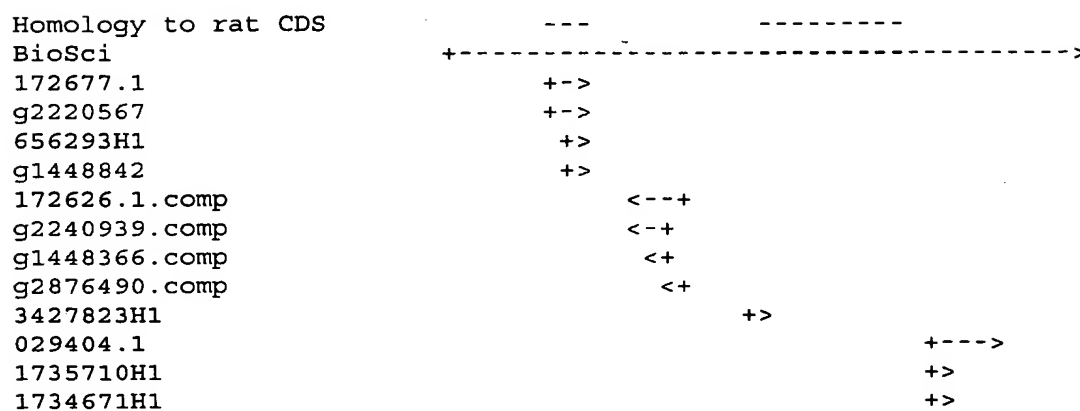


Figure 6. Full coding sequence of the human $\alpha 10$ receptor cDNA (clone D11.4)

```

+1                               M G L R S H H L S
1  GAGACCTGCC CCCGCTCTTG CAGTGCCAGG GCCATGGGGC TCCGGAGCCA CCACCTCAGC

+1 L G L L L L F L L P A E C L G A E G R L
61 CTGGGCCTTC TGCTTCTGTT TCTACTCCCT GCAGAGTGCC TGGGAGCTGA GGGCCGGCTG

+1 A L K L F R D L F A N Y T S A L R P V A
121 GCTCTCAAGC TGTTCCTGA CCTCTTGCC AACTACACAA GTGCCCTGAG ACCTGTGGCA

+1 D T D Q T L N V T L E V T L S Q I I D M
181 GACACAGACC AGACTCTGAA TGTGACCCTG GAGGTGACAC TGTCCAGAT CATCGACATG

+1 D E R N Q V L T L Y L W I R Q E W T D A
241 GATGAACGGA ACCAGGTGCT GACCCTGTAT CTGTGGATAC GGCAGGAGTG GACAGATGCC

+1 Y L R W D P N A Y G G L D A I R I P S S
301 TACCTACGAT GGGACCCCAA TGCCTATGGT GGCCTGGATG CCATCCGCAT CCCAGCAGT

+1 L V W R P D I V L Y N K A D A Q P P G S
361 CTTGTGTGGC GGCCAGACAT CGTACTCTAT AACAAAGCCG ACGCGCAGCC TCCAGGTTCC

+1 A S T N V V L R H D G A V R W D A P A I
421 GCCAGCACCA ACGTGGTCCT GCGCCACGAT GGCGCCGTGC GCTGGGACGC GCCGGCCATC

+1 T R S S C R V D V A A F P F D A Q H C G
481 ACGCGCAGCT CGTGCCGCGT GGATGTAGCA GCCTTCCCGT TCGACGCCCA GCACTGCGGC

+1 L T F G S W T H G G H Q L D V R P R G A
541 CTGACGTTTC GTCCTGGAC TCACGGCGGG CACCAACTGG ATGTGCGGCC GCGCGCGCT

+1 A A S L A D F V E N V E W R V L G M P A
601 GCAGCCAGCC TGGCGGACTT CGTGGAGAAC GTGGAGTGGC GCGTGCTGGG CATGCCGCGC

+1 R R R V L T Y G C C S E P Y P D V T F T
661 CGGCGGCGCG TGCTCACCTA CGGTGCTGC TCCGAGCCCT ACCCCGACGT CACCTTCAGC

+1 L L L R R R A A A Y V C N L L L P C V L
721 CTGCTGCTGC GCCGCCGCGC CGCCGCTAC GTGTGCAACC TGCTGCTGCC CTGCGTGCTC

+1 I S L L A P L A F H L P A D S G E K V S
781 ATCTCGCTGC TTGCGCCGCT CGCCTTCCAC CTGCCTGCCG ACTCAGGCGA GAAGGTGTGC

+1 L G V T V L L A L T V F Q L L L A E S M
841 CTGGGCGTCA CCGTGCTGCT GGCGCTCACC GTCTTCCAGT TGCTGCTGGC CGAGAGCATG

+1 P P A E S V P L I G K Y Y M A T M T M V
901 CCACCGGCCG AGAGCGTGCC GTCATCGGG AAGTACTACA TGGCCACTAT GACCATGGTC

+1 T F S T A L T I L I M N L H Y C G P S V
961 ACATTCTCAA CAGCACTCAC CATCCTTATC ATGAACCTGC ATTACTGTGG TCCCAGTGTC

+1 R P V P A W A R A L L L G H L A R G L C
1021 CGCCAGTGC CAGCCTGGGC TAGGGCCCTC CTGCTGGGAC ACCTGGCAGG GGGCCTGTGC

```

+1 V R E R G E P C G Q S R P P E L S P S P
 1081 GTGCGGGAAG GAGGGGAGCC CTGTGGGCAG TCCAGGCCAC CTGAGTTATC TCCTAGCCCC

+1 Q S P E G G A G P P A G P C H E P R C L
 1141 CAGTCGCCTG AAGGAGGGGC TGGCCCCCA GCGGGCCCTT GCCACGAGCC ACGATGTCTG

+1 C R Q E A L L H H V A T I A N T F R S H
 1201 TGCCGCCAGG AAGCCCTACT GCACCACGTA GCCACCATTG CCAATACCTT CCGCAGCCAC

+1 R A A Q R C H E D W K R L A R V M D R F
 1261 CGAGCTGCCC AGCGCTGCCA TGAGGACTGG AAGCGCCTGG CCCGTGTGAT GGACCGCTTC

+1 F L A I F F S M A L V M S L L V L V Q A
 1321 TTCCTGGCCA TCTTCTTCTC CATGGCCCTG GTCATGAGCC TCCTGGTGCT GGTGCAGGCC

+1 L
 1381 CTGTGAGGGC TGGGACTAAG TCATCTAGAG GGCCCTTCGA AGGTAAGCCT ATCCCTAACC

1441 CTCTCCTCGG TCTCGATTCT ACGCGTACCG GTCATCATCA CCATCACCAT TGAGTTTAAA

1501 C

Figure 7

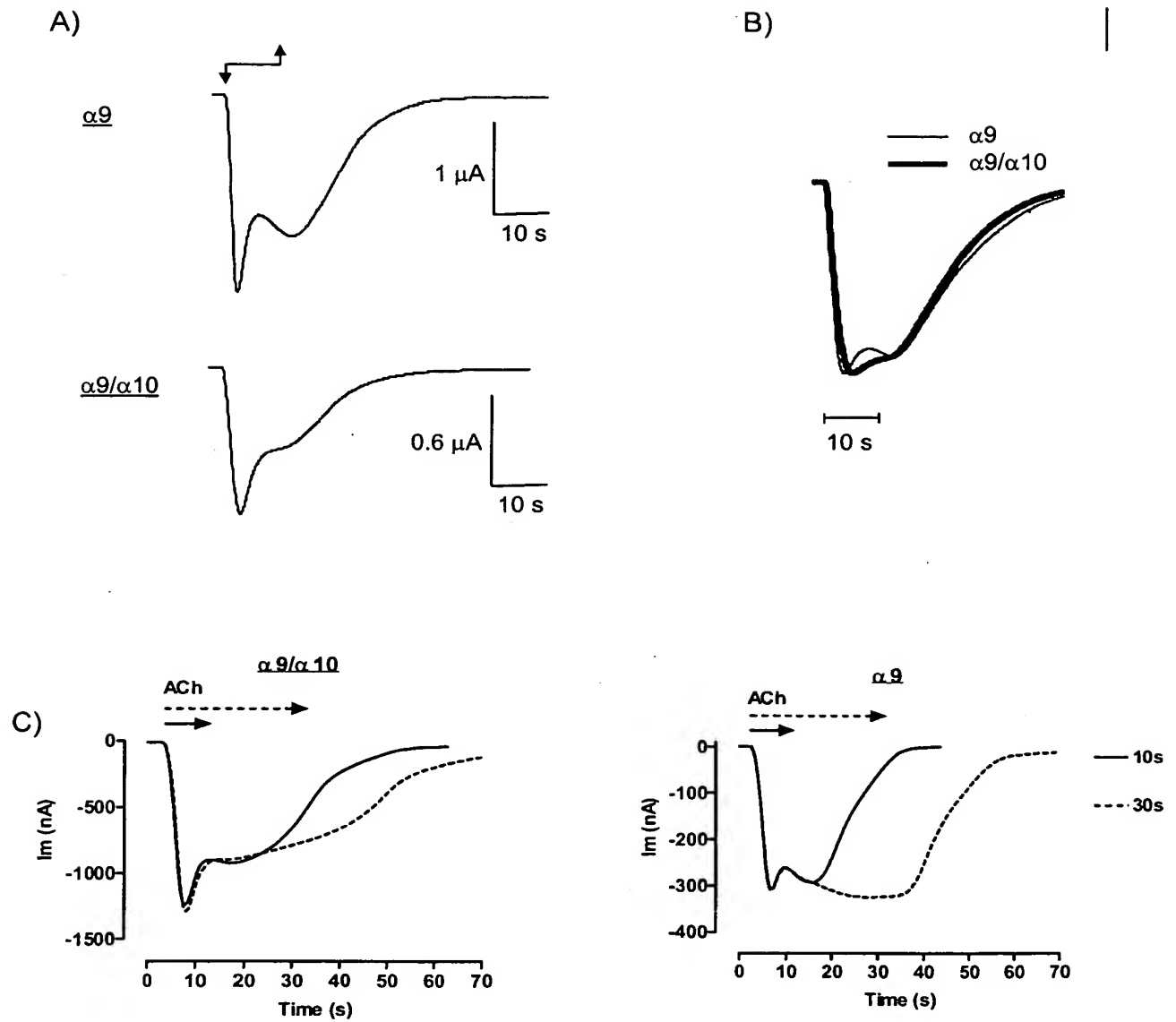


Figure 8

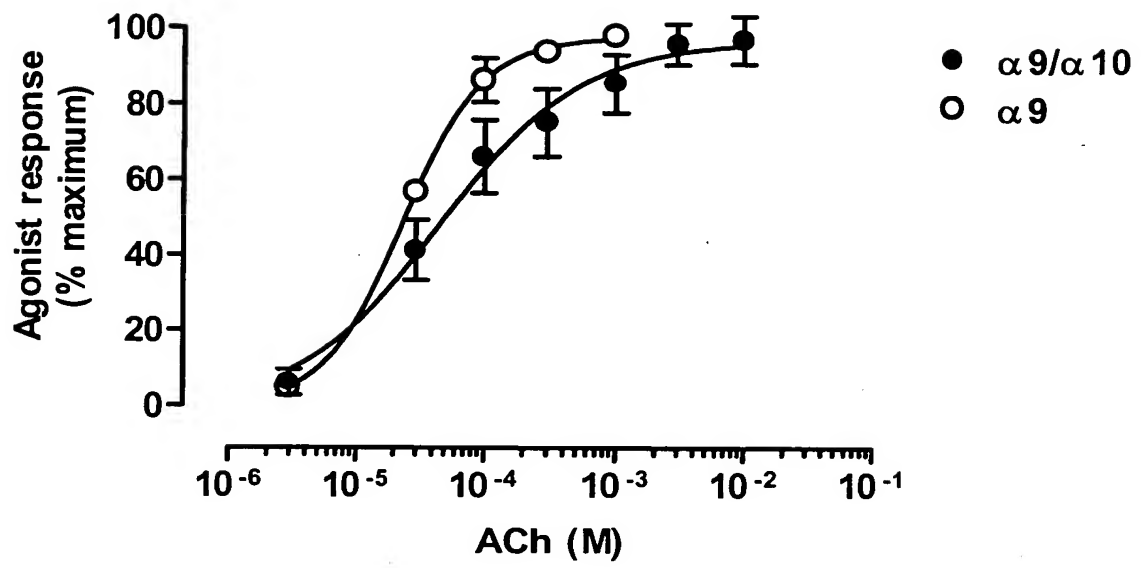


Figure 9

